MAILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.1)

type is:

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKI
VRIVDVEK
VEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.2)

(a)　Pfu pol Y7A (Y8A)

MAILDVDAITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.3)

(b)　Pfu pol Y37A (Y38A)

MAILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPAIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.4)

(c)   Pfu pol V93Q (V94Q)

MAILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDQPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.5)

(d)   Pfu pol V93R (V94R)

MAILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.6)

(e)　Pfu pol I114R (I115R)

MAILDVDAITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDRPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.7)

(f)　Pfu pol I114Q (I115Q)

MAILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPAIYALLRDDSKIEEVKKITGERHGK
IVRIVDVEK
VEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDQPFAKRYLIDKGLIPMEGE
EELKILAF
DIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKD
PDIIVTYN
GDSFDFPYLAKRAEKLGIKLTIGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPT
YTLEAVYE
AIFGKPKEKVYADEIAKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLW
DVSRSSTG
NLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPS
IIITHNVS
PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILLDY
RQKAIKLL
ANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPGG
ESEEIKKK
ALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEIAKE
TQARVLET
ILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGV
KIKPGMVI
GYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTR
QVGLTSWL
NIKKS

(SEQ ID NO.8)

(a)   Pfu pol Y7A (Y8A)

ATGGCTATCCTGGACGTTGACGCCATCACCGAAGAAGGTAAGCCGGTTATCCGTCTGTTCAA
AAAAGAAAACGGTAAATTCAAAATCGAACACGACCGTACCTTCCGTCCGTACATCTACGCTC
TGCTGCGTGACGACTCTAAAATCGAAGAAGTTAAAAAAATCACCGGTGAACGTCATGGAAAG
ATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAAAAAGTTTCTCGGCAAGCCTATTACCGT
GTGGAAACTTTATTTGGAACATCCCCAAGATGTTCCCACTATTAGAGAAAAAGTTAGAGAAC
ATCCAGCAGTTGTGGACATCTTCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGAC
AAAGGCCTAATACCAATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAAC
CCTCTATCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGATG
AAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGAGGTTGTATCA
AGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGAGAAGGATCCTGACATTAT
AGTTACTTATAATGGAGACTCATTCGACTTCCCATATTTAGCGAAAAGGGCAGAAAAACTTG
GGATTAAATTAACCATTGGAAGAGATGGAAGCGAGCCCAAGATGCAGAGAATAGGCGATATG
ACGGCTGTAGAAGTCAAGGGAAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAAT
AAATCTCCCAACATACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGA
AGGTATACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTTGCC
AAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTCCTTCCAATGGA
AATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTTCAAGGTCAAGCACAGGGA
ACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACGAAAGAAACGAAGTAGCTCCAAACAAG
CCAAGTGAAGAGGAGTATCAAAGAAGGCTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGA
GCCAGAAAAGGGGTTGTGGGAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGA
TTATAATTACCCACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGAT
ATCGCTCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTCTT
GGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACTCAAGATCCTA
TAGAAAAAATACTCCTTGACTATAGACAAAAAGCGATAAAACTCTTAGCAAATTCTTTCTAC
GGATATTATGGCTATGCAAAAGCAAGATGGTACTGTAAGGAGTGTGCTGAGAGCGTTACTGC
CTGGGGAAGAAAGTACATCGAGTTAGTATGGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAG
TCCTCTACATTGACACTGATGGTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATA
AAGAAAAAGGCTCTAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCT
TGAATATGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAATAG
ATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTGGAGTGAAATT
GCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACACGGAGATGTTGAAGAAGC
TGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGCCAATTATGAAATTCCACCAGAGAAGC
TCGCAATATATGAGCAGATAACAAGACCATTACATGAGTATAAGGCGATAGGTCCTCACGTA
GCTGTTGCAAAGAAACTAGCTGCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATA
CATAGTACTTAGAGGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATC
CCAAAAAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTACTT
AGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAGACAAGACAAGT
CGGCCTAACTTCCTGGCTTAACATTAAAAAATCC

(SEQ ID NO.9)

(b)   Pfu pol V93Q (V94Q)

ATGGCTATCCTGGACGTTGACTACATCACCGAAGAAGGTAAGCCGGTTATCCGTCTGTTCAA
AAAAGAAAACGGTAAATTCAAAATCGAACACGACCGTACCTTCCGTCCGTACATCTACGCTC
TGCTGCGTGACGACTCTAAAATCGAAGAAGTTAAAAAAATCACCGGTGAACGTCATGGAAAG
ATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAAAAAGTTTCTCGGCAAGCCTATTACCGT
GTGGAAACTTTATTTGGAACATCCCCAAGATCAGCCCACTATTAGAGAAAAAGTTAGAGAAC
ATCCAGCAGTTGTGGACATCTTCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGAC
AAAGGCCTAATACCAATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAAC
CCTCTATCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGATG
AAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGAGGTTGTATCA

AGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGAGAAGGATCCTGACATTAT
AGTTACTTATAATGGAGACTCATTCGACTTCCCATATTTAGCGAAAAGGGCAGAAAAACTTG
GGATTAAATTAACCATTGGAAGAGATGGAAGCGAGCCCAAGATGCAGAGAATAGGCGATATG
ACGGCTGTAGAAGTCAAGGGAAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAAT
AAATCTCCCAACATACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGA
AGGTATACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTTGCC
AAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTCCTTCCAATGGA
AATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTTCAAGGTCAAGCACAGGGA
ACCTTGTAGAGTGGTTCTTACTTAGGAAAGCCTACGAAAGAAACGAAGTAGCTCCAAACAAG
CCAAGTGAAGAGGAGTATCAAAGAAGGCTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGA
GCCAGAAAAGGGGTTGTGGGAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGA
TTATAATTACCCACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGAT
ATCGCTCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTCTT
GGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACTCAAGATCCTA
TAGAAAAAATACTCCTTGACTATAGACAAAAAGCGATAAAACTCTTAGCAAATTCTTTCTAC
GGATATTATGGCTATGCAAAAGCAAGATGGTACTGTAAGGAGTGTGCTGAGAGCGTTACTGC
CTGGGGAAGAAAGTACATCGAGTTAGTATGGAAGGAGCTCGAAGAAAGTTTGGATTTAAAG
TCCTCTACATTGACACTGATGGTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATA
AAGAAAAAGGCTCTAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCT
TGAATATGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAATAG
ATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTGGAGTGAAATT
GCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACACGGAGATGTTGAAGAAGC
TGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGCCAATTATGAAATTCCACCAGAGAAGC
TCGCAATATATGAGCAGATAACAAGACCATTACATGAGTATAAGGCGATAGGTCCTCACGTA
GCTGTTGCAAAGAAACTAGCTGCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATA
CATAGTACTTAGAGGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATC
CCAAAAAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTACTT
AGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAGACAAGACAAGT
CGGCCTAACTTCCTGGCTTAACATTAAAAAATCC

                                        (SEQ ID NO.10)

(c)   Pfu Pol P115Δ (P116Δ)

ATGGCTATCCTGGACGTTGACTACATCACCGAAGAAGGTAAGCCGGTTATCCGTCTGTTCAA
AAAAGAAAACGGTAAATTCAAAATCGAACACGACCGTACCTTCCGTCCGTACATCTACGCTC
TGCTGCGTGACGACTCTAAAATCGAAGAAGTTAAAAAAATCACCGGTGAACGTCATGGAAAG
ATTGTGAGAATTGTTGATGTAGAGAAGGTTGAGAAAAGTTTCTCGGCAAGCCTATTACCGT
GTGGAAACTTTATTTGGAACATCCCCAAGATGTTCCCACTATTAGAGAAAAGTTAGAGAAC
ATCCAGCAGTTGTGGACATCTTCGAATACGATATTTTTGCAAAGAGATACCTCATCGACAAA
GGCCTAATACCAATGGAGGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCT
CTATCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGATGAAA
ATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGAGGTTGTATCAAGC
GAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGAGAAGGATCCTGACATTATAGT
TACTTATAATGGAGACTCATTCGACTTCCCATATTTAGCGAAAAGGGCAGAAAAACTTGGGA
TTAAATTAACCATTGGAAGAGATGGAAGCGAGCCCAAGATGCAGAGAATAGGCGATATGACG
GCTGTAGAAGTCAAGGGAAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAATAAA
TCTCCCAACATACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGG
TATACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTTGCCAAA
TACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTCCTTCCAATGGAAAT
TCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTTCAAGGTCAAGCACAGGGAACC
TTGTAGAGTGGTTCTTACTTAGGAAAGCCTACGAAAGAAACGAAGTAGCTCCAAACAAGCCA
AGTGAAGAGGAGTATCAAAGAAGGCTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCC
AGAAAAGGGGTTGTGGGAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTA
TAATTACCCACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATC

GCTCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTCTTGGG
ACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACTCAAGATCCTATAG
AAAAAATACTCCTTGACTATAGACAAAAAGCGATAAAACTCTTAGCAAATTCTTTCTACGGA
TATTATGGCTATGCAAAAGCAAGATGGTACTGTAAGGAGTGTGCTGAGAGCGTTACTGCCTG
GGGAAGAAAGTACATCGAGTTAGTATGGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCC
TCTACATTGACACTGATGGTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAG
AAAAAGGCTCTAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGA
ATATGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAATAGATG
AAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTGGAGTGAAATTGCA
AAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACACGGAGATGTTGAAGAAGCTGT
GAGAATAGTAAAAGAAGTAATACAAAAGCTTGCCAATTATGAAATTCCACCAGAGAAGCTCG
CAATATATGAGCAGATAACAAGACCATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCT
GTTGCAAAGAAACTAGCTGCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACAT
AGTACTTAGAGGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCA
AAAAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTACTTAGG
ATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAGACAAGACAAGTCGG
CCTAACTTCCTGGCTTAACATTAAAAAATCC

(SEQ ID NO.11)

Seq id no. 12
MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTT
VRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDK
GLIPME

Seq id no.13
MKEFYLTVEQIGDSIFERYIDSNGRERTREVEYKPSLFAHCPESQATKYFDIYGKPCTRKLF
ANMRDASQWIKRMEDIGLEALGMDDFKLAYLSDTYNYEIKY

5'-GGGGATCCTCTAGAGTCGACCTGC-3' (SEQ ID NO.14))

SEQ ID NO.15
GGAGACAAGCTTGUATGCCTGCAGGTCGACTCTAGCGGCTAAAA

SEQ ID NO.17
GGAGACAAGCTTGTATGCCTGCAGGTCGACTCTAGCGGCTAAAA

(SEQ ID NO.16)
5'-hex-GCCCGCGGGAUATCGGCCCTTA-3'

Pfu (SEQ ID NO 18)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKI
VRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDK
GLIPMEG

Tgo

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTT
VRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDK
GLIPMEG

PKOD

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTV
VTVKRVEKVQKKFLGRPVEVWKLYFTHPQDVPAIRDKIREHPAVIDIYEYDIPEAKRYLIDK
GLVPMEG

DTok

MILDADYITEDGKPVIRVFKKEKGEFKIDYDRDFEPYIYALLKDDSAIEDIKKITAERHGTT
VRVTRAERVKKKFLGRPVEVWKLYFTHPQDVPAIRDKIREHPAVVDIYEYDIPFAKRYLIDR
GLIPMEG

9° N-7

MILDTDYITENGKPVIRVFKKENGEFKIEYDRTFEPYFYALLKDDSAIEDVKKVTAKRHGTV
VKVKRAEKVQKKEFLGRPIEVWKLYFNHPQDVPAIRDRIRAHPAVVDIYEYDIPFAKRYLID
KGLIPMEG

Tli

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKT
VRVLDAVKVRKKFLGREVEVWKLIFEHPQDVPAMRGKIREHPAVVDIYEYDIPFAKRYLIDK
GLIPMEG

Mvo

MDLDYNSKDLCIDMYYKNCGLKKPEINLQKECEFKPYFYVDTSEPKEIYDYLDGLNQEIDLK
KLEPEFENNTSLKVQDLITNIEIIEKIVYSDYILNGKDISEVSDFKNKKERKICKVYVKYPN
HVKIIREYFKEFGKSYEFDIPFLRRYMIDQDIVPSAK

Pis

MELKVWPLDITYAVVGSVPEIRIFGILSSGERVVLIDRSFKPYFYVDCAVCEPAALKTALSR
VAPIDDVQIVERRFLGRSKKFLKVIAKIPEDVRKLREAAMSIPRVSGVYEADIRFYMRYMID
MGVVPCSW

Afu

MERVEGWLIDADYETIGGKAVVRLWCKDDQGIFVAYDYNFDPYFYVIGVDEDILKNAATSTR
REVIKLKSFEKAQLKTLGREVEGYIVYAHHPQHVPKLRDYLSQFGDVREADIPFAYRYLIDK
DLACMDG

Csy

TVQDAVEIPPSLLVSATYDSQAGAVVLKFYEPESQKIVHWTDNTGHKPYCYTRQPPSELGEL
EGREDVLGTEQVMRHDLIADKDVPVTKITVADPLAIGGTNSEKSIRNIMDTWESDIKYYENY
LYDKSLVVGRY

Sac

```
WIKEAEDGKVYFLLQVDYDGKKSRAVCKLYDKEGKKIYIMQDESGHKPYFLTDIDPDKVNKI
TKVVRDPSFDHLELINKVDPYTGKKIRLTKIVVKDPLAVRRMRSSLPKAYEAHIKYYNNYVY
DNGLIPGLI
```

Soh

```
WIKEAEEGKSYFLLQVDYDGKKSKAICKLYDKETKKIYILYDNTGHKPYFLTDIDPEKVNKI
PKVVRDPSFDHLETVIKIDPYSGNKIKLTKIVVKDPLAVRRMRNSVPKAYEAHIKYFNNYIY
DLGLIPGLP
```

Sso

```
WLEEAQENKIYFLLQVDYDGKKGKAVCKLFDKETQKIYALYDNTGHKPYFLVDLEPDKVGKI
PKIRDPSFDHIETVSKIDPYTWNKFKLTKIVVRDPLAVRRLRNDVPKAYEAHIKYFNNYMYD
IGLIPGMP
```

Poc

```
KPLEARDGVEGFLLQTMYDGERGVAAAKIYDDRNGIVYVYFDRTGYMPYFLTDIPPDKLQEL
HEVVRHKGFDHVEVVEKFDLLRWQRRKVTKIVVKTPDVVRVLRDKVPRAWEANIKFHHNYIY
DYGLVPGMK
```

Ape

```
VREPWVESVRGYLLDVRYDGSLGKAVLMLYDPSSGSLVKWADRTGHKPYFLTDARPEDLRAA
GVDVSHDESFLQYDLVEKFHPIDRKLVKLYKIVVSDPLAVRRLREKVSSAGFSVWEADIKYH
HNYIFDRQLIPGIL
```

Amino acid motif is:

E--I-F/Y---Y-D

(SEQ ID NO.19)